

Applicant: Rajasekhar Bandaru
Title: 68730 and 69112, Protein Kinase Molecules and Uses
Therefor
USSN: 10/024,036 **Filed:** December 17, 2001
Attorney/Agent: Jean M. Silveri
Docket No.: MPI2000-521PIRM
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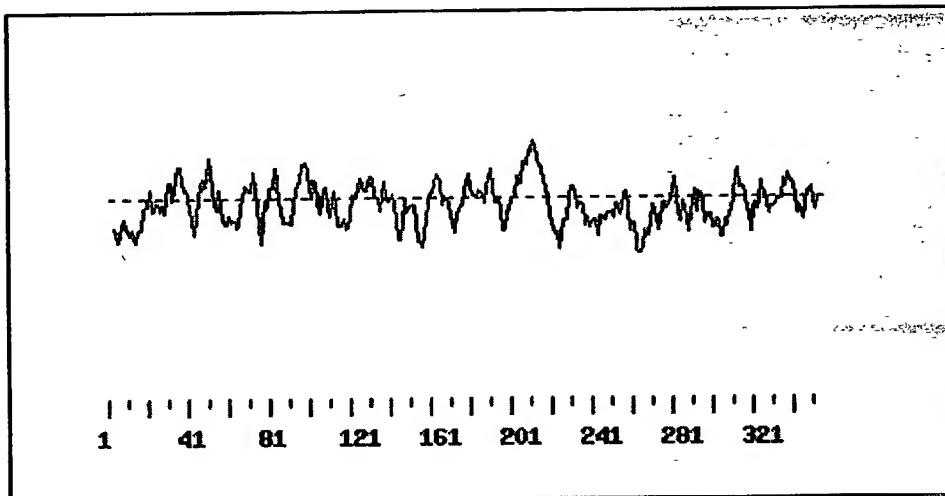


FIGURE 1

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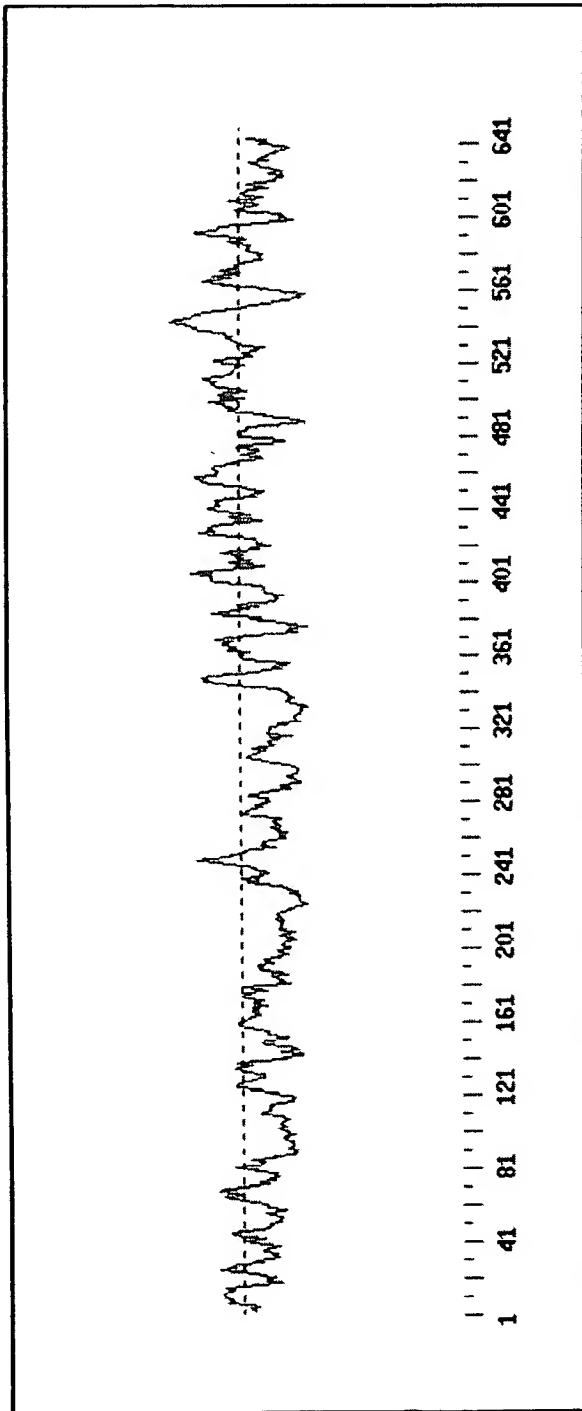


FIGURE 2

Applicant: Rajasekhar Bandaru
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USG: 10/024,636 **Filed:** December 17, 2001
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pkinase: domain 1 of 1, from 23 to 279: score 346.3, E = 3.4e-100

*->yelleklGeGsfGkVykakhk.tgkivAvKilkkesls.....lrE
+e++e+lg G+f++V +a+k tgk++AvKt++k+ l++++++ +E

68730 23 FEFKETLGTGAFSEVVLAAEKaTGKLFAVKCIPKKALKgkessiENE 69

↑
iqilkrlsHpNIVrllgvfedtddhlylvmEymegGdLfdylrngplse
i++l+++H+NIV 1 ++te ++hlylvm++ gG+Lfd+++g ++e

68730 70 IAVLRKIKHENIVALEDIYE-SPNHLYLVMQLVSGGELFDRIVEKGFYTE 118

↑
keakkialQilrGleYLHsngivHRDLKpeNILden...gtvKiaDFGL
k+a +++Q+l ++ YLH++givHRDLKpeN+L +++++ ++ i+DFGL

68730 119 KDASTLIRQVLDAYYLHRMGIVHRDLKPENLLYYSQdeesKIMISDFGL 168

↑
Arll...eklttfvGTpwYmmAPEvilegrgysskvDvWS1GviLyElit
++ ++ ++t +GTp+Y+ APEv 1 ++ys++vD WS+Gvi y ll+

68730 169 SKMEgkgDVMSTACGTPGYV-APEV-LAQKPYSKAVDCWSIGVIAYILL 216

ggplfpgadlpafggdevdqliifvlklPfsdelpktridpleelfrik
g +Pf+d ++ ++lf+ +

68730 217 G-----YPPFYD-----ENDSKLFEQI 233

kr.....rlplpsncSeelkdLlkclnkDPskRpGsatakeilnhpwf<
++ + + +p ++ +S+++kd+++ + +kDP+kR+ t++++ hpw+

68730 234 LKaeyefDSPYWDDISDSAKDFIRNLMEKDPNKRY---TCEQAARHPWI 279

-*

FIGURE 3A

Applicant: Rajasankar Banerjee

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serkin_6: domain 1 of 1, from 23 to 279: score 386.6, E = 2.5e-112

*->Yellkk1GkGaFGkVylardkktgrlvAiKvik.....erilrE

+e+ ++1G GaF++V la +k tg+l+A+K+i+++ +++++ +i++E,

68730 23 FEFKETLGTGAFSEVVLAEEKATGKLFAVKCIPkkalkgkeSSIENE 69

ikiLkk.dHPNIVkLydvd.fed.dklylVmEycceGd1GdLfdlkkrgrrg

i++L+k +H+NIV L d++e++++lylVm ++++G G+Lfd+++++g

68730 70 IAVLRKIKHENIVALEDIYESpNHLYLVMQLVSG--GELFDRIVEKGF-- 115

lrkvlsE.earfyyfrQilsaLeYLHsqgIiHRDLKPeNiLLds....hv

++E++a ++rQ+l+a+ YLH++gI+HRDLKPeN+L s+++++ +

68730 116 ----YTEkDASTLIRQVLDAVYYLHRMGIVHRDLKPENLLYYSqdeesKI 161

KlaDFG1Arql.....ttfvGTpeYmAPEvl...gYgkpavDiWS1Gci

+++DFG1++ +++ +t +GTp Y+APEvl +++Y+k avD WS+G+i

68730 162 MISDFGLSKMEdkgdvmSTACGTPGYVAPEVLaqkPYSK-AVDCWSIGVI 210

lyEl1tGkpPFp..qldlifkkig..... SpeakdLikkL

y+ll+G+pPF+++++ ++f++i++ +++ +++++++ S++akd+i++1+

68730 211 AYILLCGYPPFYdeNDSKLFEQILkaeyefdspywddiSDSAKDFIRNL 260

vkdPekRlta.eaLedeldikaHPff<-*

+kdP+kR+t++a + HP++

68730 261 EKDPNKRYTCeQAAR-----HPWI 279

FIGURE 3B

Applicant: Kajaseknar Bandaru
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Therefor
USN: 10/024,033 **Filed:** December 17, 2001
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tyrkin_6: domain 1 of 1, from 23 to 279; score 35.7, E = 4e-14

*->ltlgkkLGeGaFGeVykGt1k...ieVAVKtLkeda....keeFlrE
+++++LG GaF eV+++ k ++ AVK++ + a ++++ + +E
68730 23 FEFKETLGTGAFSEVVLAEEKatqKLFAVKCIPKKAlkgkESSIENE 69
↑
akiMkkGgkHpNiVkJLlGvcteegrrFmevePlmivmEymeqGdLldyL
+ +++k+ KH+NiV+L + ++ 1++vm +++gG L d++
68730 70 IAVLRKI--KHENIVALEDIYESP-----NHLYLVMQLVSGGELFDRI 110
↑
rknrpklslsdLlsfAlQIAkGMeYLesknfvHRDLAARNcLvgenk...
++ + +d Q+ + YL+++++vHRDL N L+ ++ +++
68730 111 -VEKGFYTEKDASTLIRQVLDAVYLYLHRMGIVHRDLKPENLLYYSQDees 159
↑↑↑↑↑↑
vvKIsDFGLsRdlyddDkkGeskdyYrkkggkggktllPirWmAPEs1kd
+ IsDFGLs+ + + d+ +++ g+ + APE+1
68730 160 KIMISDFGLSKMEGKG-----DVMSTAC--GTPG----YVAPEVLAQ 195
gkFtskSDVWSFGV1LWEift1GeqPYpgeiqqfmsneevleylkkgYRl
+ ++ + D WS GV + i+ G +P ++ +++ ++et+ k ++
68730 196 KPYSKAVDCWSIGVIAY-ILLCGYPPFYD----ENDSKLFEQILKAEYE 239
pkPendlpiSS....vtCPde1YdlM1qCWaedPedRPtFsel..verl<
++ + + + d + +lM++ dP++R t ++ ++ +
68730 240 FDSPY-----WddisDSAKDFIRNLMEK---DPNKRYTCEQAarHPWI 279

FIGURE 3C

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pkinase: domain 1 of 1, from 356 to 613: score 350.2, E = 2.3e-101

```
*->yelleklGeGsfGkVykakhk.tgkivAvKilkkesls.....lrE
     yeff++G G+f++V+++h++t + +A+Ki++k++l++++ +E
```

69112 356 YETGRVIGDGNFAVVKECRHReTRQAYAMKIIDKSRLKgkedmvDSE 402

```
iqilkrlsHpNIVrllgvfedddhlylvmEymegGdLfdylrrngplse
i i ++lsHpNIV+l+v+e td ++yl+Ey+ gGdLfd +w+w+t+e
```

69112 403 ILIIQSLSHPNIVKLHEVYE-TDMEIYLILEYVQGGDLFDAIIIESVKFPE 451

```
keakkialQilrGleYLHsngivHRDLKpeNILLden...gtvKiaDFG
++a ++ ++++l ++H++ivHRDLKpeN+L+ +n+++ t+K+aDFG
```

69112 452 PDAALMIMDLCKALVHMHDKSIVHRDLKPENLLVQRNedksTTLKLADFG 501

```
LArll.eklttfvGTpwYmmAPEvilegrgysskvDvWSlGviLyEl1tg
LA+ + + t+GTp+Y+ APE+ l+ +gy+ +vD+W+ GviLy ll+g
```

69112 502 LAKHVvRPIFTVCGTPTYV-APEI-LSEKGYGLEVDMWAAGVILYILLCG 549

```
gplfpgadlpafggdevdqliifvlklPfsdelpktridpleelfrikk
+Pf+ ++ +elf+i++
```

69112 550 -----FPPFRS-----PERDQDELFNIIQ 568

```
r.....rlplpsncSeelkdLlkkcLnkDPskRpGsatakeilnhpwf<-
++ + ++p ++n+S+++kdL+++L +DP+kR+ ta+++l+hpwt
```

69112 569 LghfefLPYYWDNISDAAKDLVSRLLVDPKKRY---TAHQVLQHPWI 613

*

FIGURE 4A

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serkin_6: domain 1 of 1, from 356 to 613: score 372.7, E = 3.8e-108

*->Yellkk1GkGaFGkVylardkktgrlvAiKvik.....erilrE
Ye +++G G F++V+ +r+++t + +A+K+i+++ +++++++ +E

69112 356 YETGRVIGDGNFAVVKECRHRETQAYAMKIIDksrlkgkeDMVDSE 402

ikILkk.dHPNIVkLydvyfed.dklylVmEyceGdlGdLfllkkrrgq
i i ++ HPNIVkL+v+e++ ++yl++Ey+ G GdLf d + + +

69112 403 ILIIQS1SHPNIVKLHEVYETdMEIYLYLEYVQG--GDLFDAAIESVK-- 448

lrkvlsE.earfyfrQilsaLeYLHsqgIiHRDLKPeNiLLds.....h
++E+a+ ++ ++aL ++H++ I+HRDLKPeN+L+ +++++++

69112 449 ---FPEpDAALMIMDLCKALVHMHDKSIVHRDLKPENLLVQRnedkstT 494

vKlaDFGlArql....ttfvGTpeYmAPEvl...gYgkpavDiWS1Gcil
+KlaDFGlA+++ ++ t++Gtp Y+APE+l++gYg +vD+W+ G+il

69112 495 LKLADFGLAHVvrpiFTVCGTPTYVAPEILsekGYGL-EVDMWAAGVIL 543

yElltGkpPFp....qldifkkig.....SpeakdLikkl
y+ll+G pPF++++++d++f++i ++ + +++++ S+ akdL+++

69112 544 YILLCGFPFRsperDQDEFNIIQ1ghfeflpwywdniSDAAKDLVSRL 593

LvkdkPekRlta.eaLedeldikaHPff<-*
Lv+dP+kR+ta+++L+ HP++

69112 594 LVVDPKKRYTAhQVLQ-----HPWI 613

FIGURE 4B

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tyrkin_6: domain 1 of 1, from 356 to 613: score 50.0, E = 5.3e-15
 *-->ltlgkkLGeGaFGeVykGtlk...ieVAVKtLkeda....keeFlre
 + g+++G G+F +V +++ +++++ A K + ++ ++++ + +E
 69112 356 YETGRVIGDGNFAVVKECRHRetrQAYAMKIIDKSR1kgkEDMVDSE 402
 akiMkklGgkHpNiVvkLlGvcteeGrrFmevePlmivmEymegGdLldyl
 + i +l +HpNiVkl+ v ++ . . . +++++Ey+ gGdL d +
 69112 403 ILIIQSL--SHPNIVKLHEVYETD-----MEIYLILEYVQGGDLFDAl 443
 rknrpklslsdLlsfAlQIAkGMeYLesknfvHRDLAARNcLvgenk...
 ++ + ++ +d + + +k + ++k +vHRDL N Lv +n +++
 69112 444 IESVK-FPEPDAALMIMDLCKALVHMHDKSIVHRDLKPENLLVQRNEdks 492
 .vvKIsDFGLsRdlyddDkkGeskdyYrkkgggkgtllPirWmAPEs1k
 ++ K +DFGL++ + ++ +g APE 1
 69112 493 tTlKLADFGLAHKVVVRP-----IFTV---CGTP---TYVAPEILS 526
 dgkFtskSDVWSFGV1LWEiftlGeqPYpgeiqqfmsneeVleylkGyr
 ++ + + D W+ GV L+ i+ G +P ++ + +e+++ ++ G+
 69112 527 EKGYGLEVDMWAAAGVILY-ILLCGFPFRSPE--RDQDELFNIIQLGHF 572
 lpkPendlpiSsvtCPdelYdlM1qCWaedPedRPtFsel..verl<-*
 P++ +d+ dl ++ dP++R t ++ ++ +
 69112 573 EFLPPY----WDNISDAAKDLVSRLLVDPKKRYTAHQVlqHPWI 613

FIGURE 4C